

	1	10	20	30	40	50	60	70	80	90	100																																																																																					
	1	MSQRP	TFYQEL	NKTI	MEVPER	YNLS	SPVGS	GAYG	SVCA	AFDT	KTHRV	AVVK	LSAP	PFQ	SI	IHKRT	YREL	RL	KKH	KHEN	VIGL	LDV	FT	PAR	SLEE	FN																																																																						
		MSHSP	SLPT	QT	CGA	--	MEM	KER	-----	LG	TGG	FN	VR	WH	NQ	VT	GE	IA	IK	QC	RQ	EL	--	SP	KNR	DR	MC	LE	IQ	IM	RR	L	N	HP	VV	AR	DR	V	PE	GR	N	L	AP	ND																																																				
		mqer	P	slpr	Dec	na	..	ME	KER	LG	S	G	a	%	G	n	V	ca	ah	#	q	k	T	G	e	r	..	SI	i	na	d	R	t	c	r	E	i	r	..	\$	n	H	e	n	V	l	a	a	r	D	V	f	e	g	a	r	n	L	a	e	n	#																																	
	101	110	120	130	140	150	160	170	180	190	200																																																																																					
	1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																																																																					
		DVYL	V	THL	M	G	A	D	L	----	N	N	I	V	K	C	Q	K	L	T	D	H	V	Q	F	L	I	Y	Q	I	L	R	G	L	K	Y	I	H	S	A	D	I	I	H	R	L	K	P	S	N	L	A	V	N	E	D	C	E	L	----	K	I	L	D	F	G	L	A	R	H	T	D	D	E	M	----	T	G	V	A	T	R	W	Y	R	A										
		L	P	L	A	M	E	Y	C	Q	G	D	L	R	R	Y	L	N	O	F	E	N	C	C	G	L	R	E	G	A	I	L	T	L	S	O	I	A	S	A	L	R	Y	L	H	E	N	R	I	I	H	R	L	K	P	E	N	I	V	L	Q	Q	E	K	R	L	I	A	K	I	I	D	L	G	Y	A	K	E	L	D	G	S	L	C	T	S	F	V	G	T	L	Q	Y	L	A	
		.dl	l	a	n	e	h	c	q	G	a	D	L	...	N	#	i	e	n	C	c	g	L	r	#	d	a	!	q	f	L	i	s	!	a	r	a	L	r	Y	I	H	e	a	r	I	I	H	R	L	K	P	e	n	i	a	l	#	d	c	e	r	...	K	I	I	D	L	G	L	A	r	e	l	D	#	e	n	...	I	g	x	V	a	t	r	q	y	r	a						
	201	210	220	230	240	250	260	270	280	290	300																																																																																					
	1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																																																																					
		P	E	T	M	L	N	M	H	Y	N	O	T	V	D	I	N	S	V	G	C	I	M	A	E	L	L	I	G	--	R	T	L	F	P	G	I	O	H	I	D	----	Q	L	K	I	L	R	L	V	G	T	P	G	A	E	L	L	K	I	S	S	E	S	A	--	R	N	Y	I	Q	S	L	A	Q	M	P	K	H	N	F	A	N	V	I	G	A	N	P	L	A	V	O			
		P	E	L	--	L	E	Q	K	Y	T	V	T	D	I	N	S	F	G	L	A	F	E	C	I	I	G	E	R	P	F	L	P	N	H	Q	P	V	Q	N	H	S	K	V	R	O	K	S	E	V	D	I	V	S	E	D	L	N	G	I	V	K	F	S	S	S	S	P	P	N	N	I	N	S	V	L	A	E	R	L	E	K	H	L	Q	L	M	L	T	H	Q	P	R	Q	R	G
		P	E	I	.	L	#	q	q	h	y	n	q	I	V	D	I	N	S	f	g	e	i	a	a	E	c	i	t	G	.	R	p	l	P	n	t	#	i	!	r	q	k	e	l	r	i	v	g	s	e	d	a	#	g	k	k	I	S	S	e	S	a	.	r	N	n	i	!	S	L	a	a	e	r	i	e	n	f	a	!	n	i	g	e	a	#	P	r	a	r	d			
	301	310	320	330	340	350	360	370	380	390																																																																																						
	1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																																																																					
		L	L	E	K	----	M	L	V	O	S	O	K	R	I	T	A	Q	A	L	----	A	H	A	Y	F	A	Q	Y	H	O	P	O	E	P	V	A	D	P	Y	D	Q	S	F	E	S	R	O	L	L	I	D	E	N	K	S	L	T	Y	D	E	V	I	S	F	V	P	P	L	D	Q	E	E	M	E	S																				
		V	D	P	Q	Y	G	P	N	G	C	F	R	A	L	D	O	I	L	N	L	K	V	H	I	L	N	M	V	T	G	I	T	H	T	P	V	M	E	O	E	S	L	Q	S	L	K	T	R	I	E	D	T	G	I	L	E	T	D	Q	E	L	L	Q	E	A	G	L	V	L	L	P	D	K	P	A	T	Q	C	I	S	O	S	K	T	N	E	G								
		I	d	e	q	n	r	a	L	o	d	d	r	i	k	a	a	q	a	l	...	a	h	a	t	.	i	a	q	Y	h	d	n	#	D	E	p	l	a	d	k	d	r	i	r	E	d	r	d	i	l	e	d	#	q	e	l	l	q	e	a	e	l	l	l	p	d	k	P	a	d	Q	c	e	n	#	S																	

Fig. 1(a)

	1	10	20	30	40	50	60	70	80	90	100
P38	1										
MEK-1	MPKKKPTPIQLNPAPOGSAVNGTSSAETNLEALQKKLEELEDEORAKRLEFLQKKVGELODDFEKISELGAGNGGVVEKYSKPSGLYMARKLTH										
Consensus										
	101	110	120	130	140	150	160	170	180	190	200
P38	1										
MEK-1	PFQSIHAKRTYRELRLKMKHENVIGLLDVFTPARSLEEFNDVYLVIHMGADLNNIVK-CQKLTDDHVDFELYQILRELKYIHSAD-IHRODKPS										
Consensus	reiqpaIr..nrliRELrllhecnhenlilglldaFtparale.....lcnchsdGadL#lIk.eqrlp##hlqkllalaIrGlkyIread.IHRODKPS										
	201	210	220	230	240	250	260	270	280	290	300
P38	1										
MEK-1	NLAVNEOCELKTLDFGLARNTODEMIG-YVATRMVYRAPEIMLNHMYNQTVQIHSVCIMAEELLTGRILFPGTDHIOQLKTLRLVGPGEALLKKISSE										
Consensus	NILVNSRGEIKLCOFGVSGQLIDSMANSFVGTIRSYNSPE-RLQGTIVSYVQSDIHSNGLSLVEMVRGYPPIPPDAKELELLFCQVEGDARELTPPRPRTP										
	301	310	320	330	340	350	360	370	380	390	400
P38	1										
MEK-1	SARNYIQSLRQMPKKN-FANVFIGANPLAYDOLLEKMLVDSOKRTTAAQALAHAYEAGYHDPPDEPVADPYQDSFESROLLIDENKSLTYDEVTSFVPPP										
Consensus	GRPLSSYGMDSRPPPHAIPELLDYIVNEPPKLPSSGVESLEFQDFVKNCLKNPACRADLK---GLMVHAFIKSDRAEVDFAENLCSTIIGLNQPSIPTH										
	401	408									
P38	1										
MEK-1	garnelqgagqrPkMa.FanldigaNelapdllegnlal.f#dr!naaqalahRerf8lh.....#lnadaxdqrf#ar#ldlaaHlcllIdenqftPph										
Consensus										

Fig. 1(b)

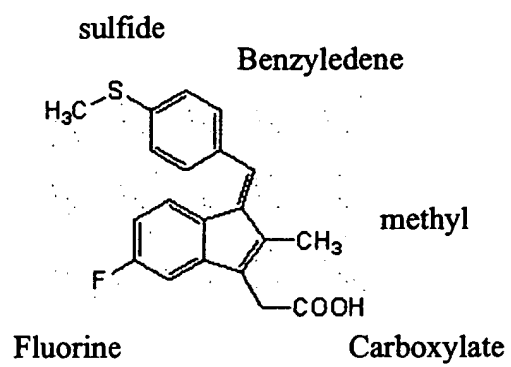


Fig. 2(a)

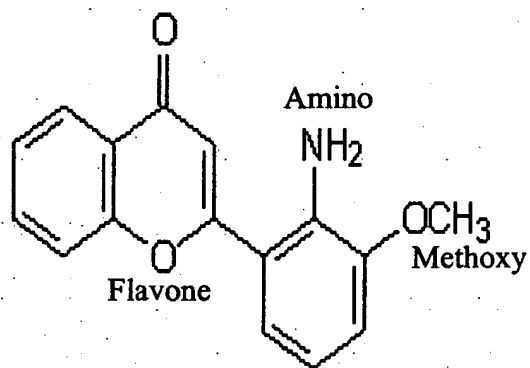


Fig. 2(b)

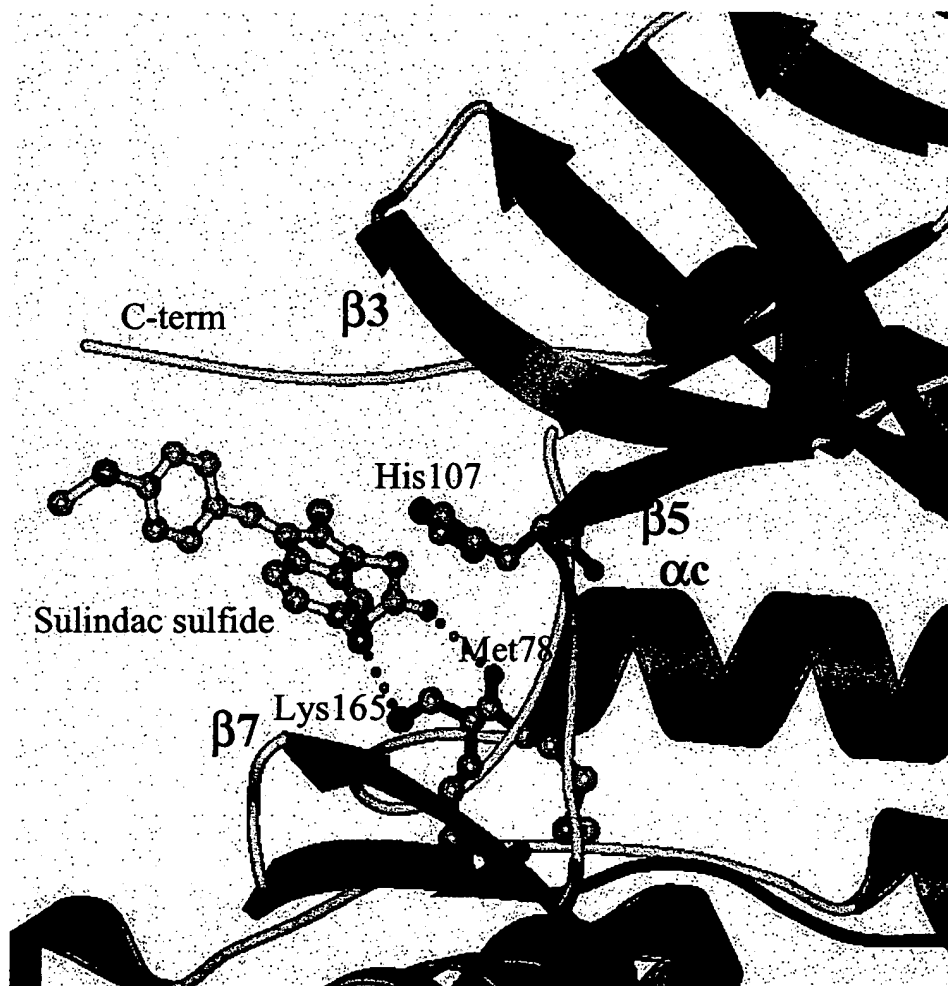


Fig. 3(a)

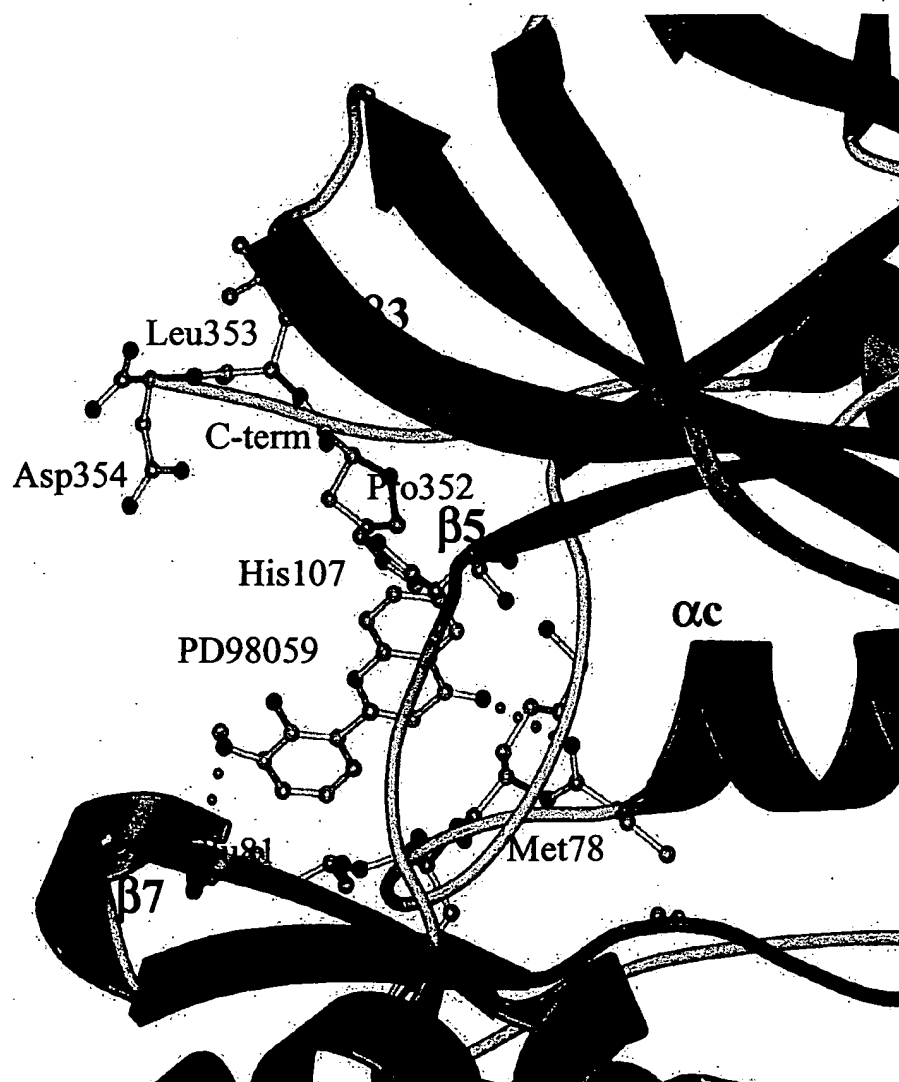


Fig. 3(b)

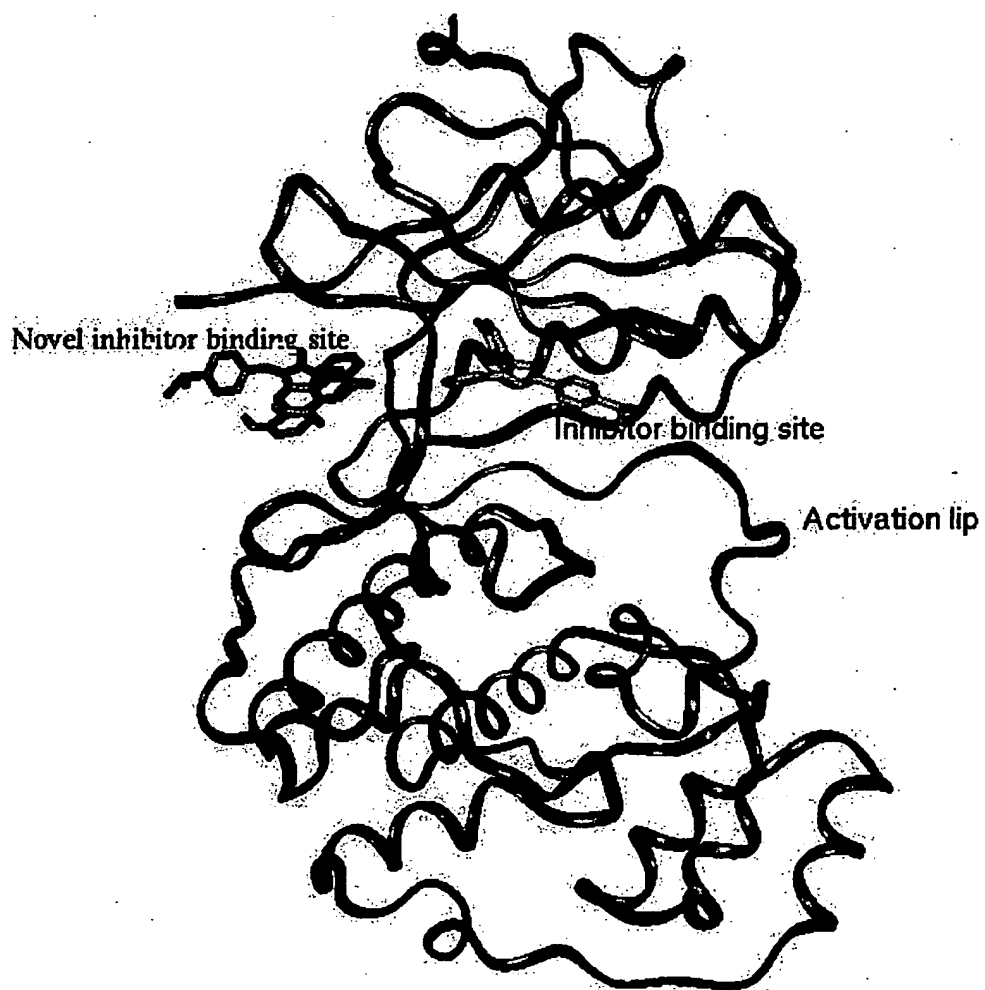


Fig. 4

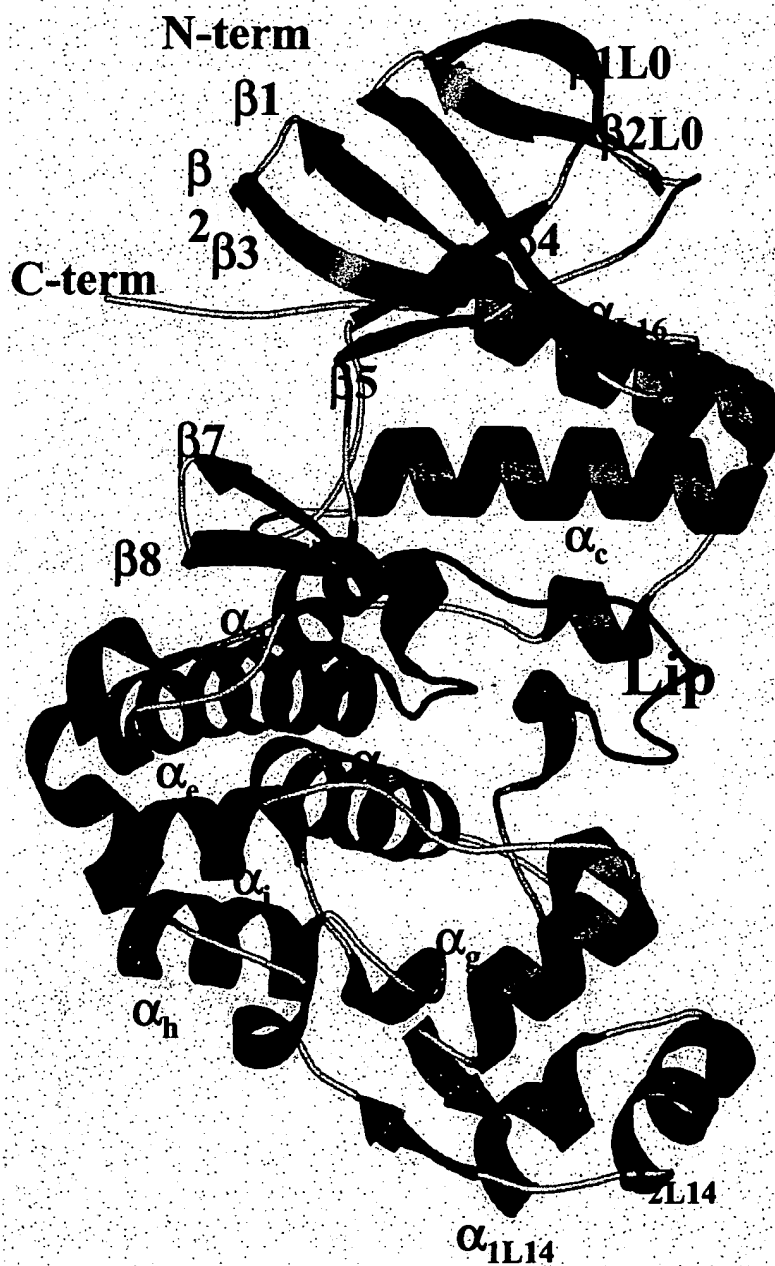


Fig. 5

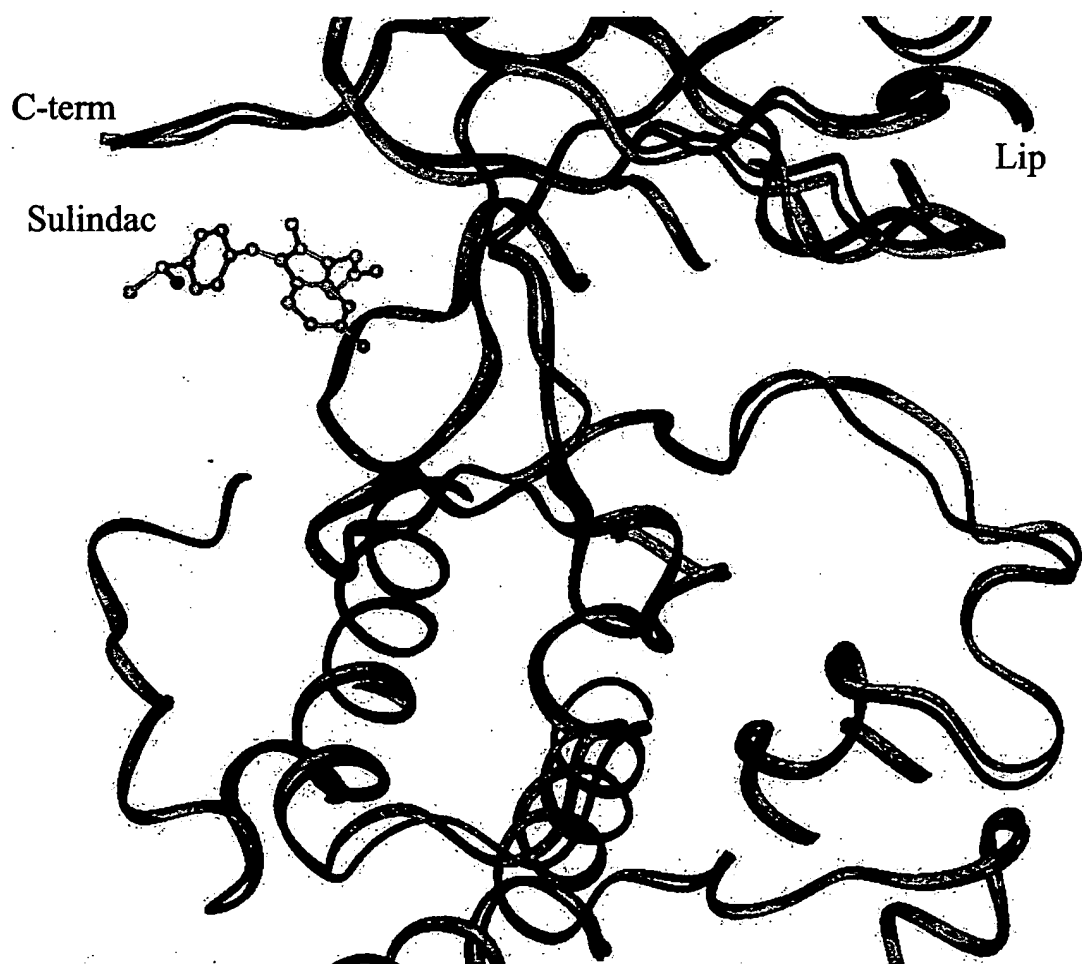


Fig. 6

Linker 2

P38	25	Q N L S - - - - - P V G S G A <u>Y</u> G S V C - - - - - A A F
IKK	21	- - - - - L G T G G <u>F</u> G N V I - - - - - R W H
MEK1	69	E K I S - - - - - E L G A G N G G V V F - - - - - K V S
JNK3	27	Q N L K - - - - - P I G S G A <u>Q</u> G I V C - - - - - A A Y
GSK3	52	Q E V S Y T D T K V I G N G S <u>F</u> G V V Y - - - - - Q A K
Akt	153	D Y L K - - - - - L L G K G T <u>F</u> G K V I - - - - - L V R
NIK	446	R D L T - - - - - E N V N G M A M N L T T Q V R E I A K V

Helix C

P38	63	I H A K R T Y R E L - - - - - R L <u>L</u> K H
IKK	53	K N R D R W C L E I - - - - - Q I M R R
MEK1	107	I R - N Q I I R E L - - - - - Q V <u>L</u> H E
JNK3	65	T H A K R A Y R E L - - - - - V L <u>M</u> K C
GSK3	91	- - K R F K N R E L - - - - - Q I <u>M</u> R K
Akt	192	D E V A H T V T E S - - - - - R V <u>L</u> Q N
NIK	491	L D L K N T I N T M V D R L G T F A F E V S K V

Linker 5

P38	78	M <u>K</u> H <u>E</u> N V I G
IKK	68	L N H <u>P</u> N V V A
MEK1	121	C <u>N</u> S <u>P</u> Y I V G
JNK3	80	V N H <u>K</u> N I I S
GSK3	104	L D H C N I V R
Akt	207	T R H <u>P</u> F L T A
NIK	515	A R E <u>V</u> G T D G

Crossover

P38	100	N - D V Y L V <u>T</u> <u>H</u> L M G A D L - - - - N - N
IKK	90	D L P L L A M E <u>Y</u> C Q G G D L R R Y L N - Q
MEK1	142	- - - - I C M E <u>H</u> M D G G S L - - - - D - Q
JNK3	102	Q - D V Y L V <u>M</u> <u>E</u> L M D A N L - - - - C - Q
GSK3	119	V - Y L N L V L <u>D</u> Y V P E T V - - - - Y - R
Akt	226	- - - C F V M E <u>Y</u> A N G G D L - - - - F F H
NIK	538	K - D L T E N V N T M A S N L - - - - T - S

C-Terminus

P38	345	V I S F V P P P L D Q E
IKK	359	L V L L P D K P A T Q C
MEK1	385	N Q P S T P T H A A S I
JNK3	363	V M N S E - - - - -
GSK3	374	A T I L I P P H A R I Q
Akt	464	L D Q R T H F P Q F S Y
NIK	788	V F N A L K T L A V K E

Fig. 7